

NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN MUTATED FORM WITH
AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL DYSTROPHY (APECED)

The present invention relates to a nucleic acid molecule encoding a (poly)peptide co-segregating in mutated form with Autoimmune Polyendocrinopathy Candidiasis Ectodermal Dystrophy (APECED). In addition, the present invention relates to a mammalian, preferably murine, homologue of the above nucleic acid molecule. The present invention further relates to a nucleic acid molecule deviating by at least one mutation from the nucleic acid molecule described above wherein said mutation co-segregates with APECED and is an insertion, a deletion, a substitution and/or an inversion, and wherein said mutation further results in a loss or a gain of function of the (poly)peptide encoded by said mutated nucleic acid molecule. Furthermore, the present invention relates to a vector comprising the nucleic acid molecules described above and to a host transformed with said vector. In addition, the present invention relates to a process of recombinantly producing a (poly)peptide encoded by the nucleic acid molecules described above comprising culturing or raising said host and isolating said (poly)peptide from said culture or said host. The present invention further relates to the (poly)peptide encoded by said nucleic acid molecules or produced by the process described above. Additionally, the present invention relates to an antibody that specifically recognizes said (poly)peptides. Moreover, the present invention relates to a method for testing for a carriership for APECED or for a corresponding disease state comprising testing a sample obtained from a prospective patient or from a person suspected of carrying a predisposition for a mutation in the wild-type nucleic acid molecule described above or a mutated form of the (poly)peptide encoded by said mutated nucleic acid molecule in an immuno-assay using the antibody described above.

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Self tolerance and the ability to discriminate between self and non-self antigens are central to the immune response. Autoimmunity develops following a loss of self tolerance. There are several hypotheses which have been suggested, reflecting possible mechanisms leading to an autoimmune response: These hypotheses comprise:

- Presentation of sequestered self antigens: immunological tolerance is not established when molecules of the body are hidden from the lymphoreticular system (e.g. in the lens of the eye, in sperm or the heart). If the tissues are damaged, an autoimmune response can develop.
- Cross-reactivity: in the case when a self antigen and an exogenous antigen cross-react, the shared epitope is presented to the immune system with a different carrier, allowing T helper cells to confer a signal to B cells with antibody receptors recognizing the epitope.
- Modification of auto-antigens: a modification of an auto-antigen may arise and if different, this altered antigen could be recognized as foreign and trigger an immune response.
- Viral infections: auto-antibodies can sometimes arise following viral infections.
- Ectopic expression of HLA class II antigens: class II antigens have a restricted tissue distribution. The tissues affected in autoimmune diseases may express class II antigens inappropriately.
- Regulatory defects: (1) T cells sometimes recognize self-antigens but fail to co-operate with B cells due to peripheral tolerance exerted by suppressor T cells. A failure in this regulatory mechanism could result in autoimmunity. (2) Polyclonal B cell activation: some molecules can mimic the T cell stimulus and activate B cells to divide polyclonally. This could lead to the activation of B cells secreting auto-antibodies.

There is a wide range of autoimmune diseases. The spectrum spans conditions involving a single organ through those involving all systems in the body. Autoimmune diseases are characterized by an abnormal response of the human immune system to self components. The impact of these diseases on health of populations is high since many common diseases like diabetes mellitus, multiple sclerosis or rheumatoid arthritis represent autoimmune reactions. Consequently, characterization of molecules involved in autoimmunity are of high importance for the cure and treatment of these disorders.

Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED, OMIM 240300) is an autosomal recessive disease characterized by 1) autoimmune polyendocrinopathies:

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hypoparathyroidism, adrenocortical failure, IDDM, gonadal failure, hypothyroidism, pernicious anemia, and hepatitis, 2) chronic mucocutaneous candidiasis and 3) ectodermal dystrophies: vitiligo, alopecia, keratopathy, dystrophy of dental enamel, nails and tympanic membranes (Ahonen, P., et al., *N. Engl. J. Med.*, **322**, 1829-1836 (1990)). The disease is reported worldwide but is exceptionally prevalent among the Finnish population (incidence 1: 25 000) and the Iranian Jews (Ahonen, P., et al., *N. Engl. J. Med.*, **322**, 1829-1836 (1990); Zlotogora, J., et al., *J. Med. Genet.*, **29**, 824-826 (1992)). The primary biochemical defect in this disorder remains elusive.

APECED is the only described systemic autoimmune disease in humans with Mendelian inheritance, and the clinical phenotype characterized by autoimmune endocrinopathies, including IDDM, and chronic candidiasis would suggest defects in both humoral (Ahonen, P., et al., *J. Clin. Endocrinology and Metabolism*, **64**, 494-500 (1987)) and cell mediated immunity (Fidel, P. L. & Sobel, J. D., *TIMB*, **2**, 202-206 (1994)). No single HLA associated haplotype exists (Ahonen, P., et al., *J. Clin. Endocrinology and Metabolism*, **66**, 1152-1157 (1988)), autoantibodies are found against several cell types in the patients' sera (Ahonen, P., et al., *J. Clin. Endocrinology and Metabolism*, **64**, 494-500 (1987)) and only unspecific abnormal responses have been found in T cell proliferation tests. These observations would suggest a deregulation of both B and T cell specific immune responses in APECED. Moreover, the non-specific autoantibodies detected in the APECED patients' sera against several cell types do not support the hypothesis of one major autoantigen (Krohn, K., et al., *Lancet*, **339**, 770-773 (1992)). However, despite these well defined characteristics, the etiology of APECED, like of most autoimmune diseases, remains unknown. Insights into said etiology would also provide an entry point for the dissection of molecular mechanisms leading to the development of autoimmunity in general. On the basis of such knowledge, means and methods for the prevention or treatment of autoimmune diseases in general and APECED in particular might be developed.

Accordingly, the technical problem underlying the present invention was to uncover factors involved in the development of APECED that might contribute to providing means of treating or curing monogenic autoimmune diseases, in particular APECED.

The solution to the above technical problem is achieved by providing the embodiments characterized in the claims.

Accordingly, in one aspect the present invention relates to a nucleic acid molecule encoding a (poly)peptide co-segregating in mutated form with Autoimmune Polyendocrinopathy Candidiasis Ectodermal Dystrophy (APECED) which is

- (a) a nucleic acid molecule comprising a nucleic acid molecule encoding the (poly)peptide having the amino acid sequence of Fig. 2A;
- (b) a nucleic acid molecule comprising the nucleic acid molecule having the nucleotide sequence of Fig. 2A that encodes the amino acid sequence of Fig. 2A;
- (c) a nucleic acid molecule hybridizing to the nucleic acid molecule of (a) or (b); or
- (d) a nucleic acid molecule which is degenerate to the nucleic acid molecule of (c).

The present invention surprisingly revealed that a novel polypeptide, designated APGD1 for autoimmune polyglandular disease type 1, encoded by the nucleic acid molecule of the invention co-segregates in mutated form with APECED. As used throughout the present specification the term "APGD1" and the term "AIRE" denote the same (poly)peptide and are used interchangeably.

As used herein, the term "co-segregation" relates to any association of the mutated form of the polypeptide with APECED. APGD1 is a protein with a predicted length of 545 amino acids, a theoretical molecular weight of 57,7 kD and a calculated pI of 7,53. Statistical analysis of the protein sequence of Fig. 2A (Brendel, V., et al., *Proc. Natl. Acad. Sci. USA*, 89, 2002-2006 (1992)) indicates a high content of proline (11.7%) but no apparent clusters of charged amino acids or periodicity patterns. The secondary structural content of APGD1 was predicted to consist mostly of coils, with only a weak probability for the occurrence of structural α -helices or β -sheets. A putative bi-partite nuclear targeting signal (Dingwall, C. & Laskey R. A., *TIBS*, 16, 478-481 (1991)) was found between amino acids 113 to 133 (Figure 2A). The predicted protein harbors two cysteine-rich regions of 42 amino acids, each specifying a Cys4-His-Cys3 double-paired finger motif similar to the PHD finger type (Aasland, R., et al., *TIBS*, 20, 56-59 (1995)) (Figure 2A). Spacing of essential residues is conserved in the two motifs found in APGD1:

C_{299,434}-XX-C_{302,437}-X(8)-C_{311,446}-XX-C_{314,449}-X(4)-H_{319,454}-XX-C_{322,457}-X(14)-C_{337,471}-XX-C_{340,474}

(where X is any amino acid and numbers in parenthesis represent the length of the intervening peptide sequence). This structural motif has been reported for a number of nuclear proteins involved in the mediation or regulation of transcription, such as TIF1 (Transcription Intermediary Factor 1) (Douarin, Le, B., et al., *EMBO J.*, **14**, 2020-2033 (1995)) and KRIP-1 (KRAB-A Interacting Protein) (Kim, S-S., et al., *Proc. Natl. Acad. Sci. USA*, **13**, 15299-14304 (1996)). Sequence homology of APGD1 with other proteins in the databases was strictly limited to this Cys4-His-Cys3 motif. Although the spacing of residues is conserved in each case, the sequence is most closely homologous to the Mi-2 autoantigen (Ge, Q., et al., *J. Clin. Invest.*, **96**, 1730-1737 (1995)) and the TIF1 proteins (Thenot, S., et al., *J. Biol. Chem.*, **272**, 12062-12068 (1997)). Mi-2 is the major nuclear antigen detected in the sera of autoimmune dermatomyositis patients (Ge, Q., et al., *J. Clin. Invest.*, **96**, 1730-1737 (1995)) and TIF1 is involved in the transcriptional control of the estrogen receptor (Thenot, S., et al., *J. Biol. Chem.*, **272**, 12062-12068 (1997)).

By the provision of the nucleotide acid molecule of the invention it is now possible to isolate identical or similar nucleic acid molecules which code for proteins with identical functions and characteristics and which are derived from other individuals or which represent alleles of the nucleic acid molecule of the invention. Well-established approaches for the identification and isolation of such related sequences are, e.g., the isolation from genomic or cDNA libraries using the complete part of the disclosed sequence as a probe or the amplification of corresponding nucleic acid molecules by polymerase chain reaction using specific primers.

As stated hereinabove, the invention also relates to nucleic acid molecules which hybridize to the above described nucleic acid molecules and differ at one or more positions in comparison to these as long as they encode a (poly)peptide having the above described characteristics. In connection with the present invention, the term "hybridizing" is understood as referring to conventional hybridization conditions, preferably such as hybridization in 50% formamide, 6x SSC, 0.1% SDS, and 100µg/ml ssDNA, in which temperatures for hybridization are above 37°C and temperatures for washing in 0.1x SSC, 0.1% SDS are above 55°C. Most preferably, the term "hybridizing" refers to stringent hybridization conditions, for example such as described in Sambrook, et al. (Molecular cloning; A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor NY (1989)) or Higgins & Hames

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(Nucleic acid hybridization, A practical approach, IRL Press, Oxford (1985)). Said nucleic acid molecules comprise those which differ, for example, by deletion(s), insertion(s), alteration(s) or any other modification known in the art in comparison to the above described nucleic acid molecules. Methods for introducing such modifications in the nucleic acid molecules according to the invention are well-known to the person skilled in the art; see, e.g., Sambrook, et al., supra.

As mentioned hereinabove, the invention also relates to nucleic acid molecules the sequence of which differs from the sequence of the above-described hybridizing molecules due to the degeneracy of the genetic code.

In a preferred embodiment of the nucleic acid molecule of the present invention, said (poly)peptide has the function of a transcription factor or a transcription-associated factor. As used herein, the term "transcription factor" or "transcription-associated factor" comprises any factor which directly or indirectly influences transcription of a gene by, e.g., directly interacting with regulatory sequences, interacting with other transcription regulating factors, changing the conformation of chromatin, and the like.

The (poly)peptide encoded by the nucleic acid molecule of the invention preferably comprises at least one zinc finger motif. The term "zinc finger" describes a certain amino acid motif, which is able to bind metal ions, and is well known for those skilled in the art. Preferably, the (poly)peptide of the invention comprises two double-paired zinc finger motifs. Comprised by the present inventions are furthermore embodiments of nucleic acid molecules that specify polymorphisms of the above identified locus which correlate with APECED. Said polymorphisms may or may not lead to amino acid substitutions. Polymorphisms can be tested for according to conventional procedures.

In yet another aspect, the present invention relates to a mammalian homologue of the nucleic acid molecule(s) of the present invention. The person skilled in the art knows on the basis of the teachings of the present invention how to obtain the homologue, e.g., of other mammals such as mouse, rat, rabbit or pig. This can be effected, e.g., by hybridization of the molecule of the present invention under low stringent conditions to the corresponding nucleic acids

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from other species contained, e.g., in conventional libraries. "Low stringent conditions" differ from stringent conditions (described hereinabove) in that higher salt concentrations and/or lower temperatures are employed for hybridization. Such conditions are well known in the art (see, e.g., Sambrook et al. or Higgins & Hames, *supra*).

In a preferred embodiment said mammalian homologue is a murine homologue.

In a most preferred embodiment said murine homologue is a nucleic acid molecule which is

- (a) a nucleic acid molecule comprising a nucleic acid molecule encoding the (poly)peptide having the amino acid sequence of Fig. 14;
- (b) a nucleic acid molecule comprising the nucleic acid molecule having the nucleotide sequence of Fig. 14 that encodes the amino acid sequence of Fig. 14;
- (c) a nucleic acid molecule hybridizing to the nucleic acid molecule of (a) or (b); or
- (d) a nucleic acid molecule which is degenerate to the nucleic acid molecule of (c).

The murine homologue of the nucleic acid molecule of the present invention may be advantageously used to develop an animal model for APECED. Based on this animal model it is envisaged in accordance with the present invention to dissect the events which lead to the development of APECED. This may ultimately lead to the development of e.g. pharmaceutical compositions for preventing and/or treating this autoimmune disease.

In a further embodiment, the present invention relates to a nucleic acid molecule deviating by at least one mutation from the nucleic acid molecules described above, wherein said mutation co-segregates with APECED and is

- (a) an insertion;
- (b) a deletion;
- (c) a substitution; and/or
- (d) an inversion,

and wherein said mutation further results in a loss of function or a gain of function of the (poly)peptide of the invention.

Especially with respect to insertions and deletions, it could be shown in accordance with the present invention that such mutations may lead to a frame shift which in turn leads to the expression of a truncated form of the (poly)peptide of the present invention.

The term "substitution", as used herein, also includes point mutations resulting in an amino acid exchange. Examples of specific point mutations are given herein below. However, such point mutations may also lead to the creation of nonsense codons, i.e. stop codons, which lead to premature termination of translation and, thus, to truncated forms of the (poly)peptide of the present invention.

In a preferred embodiment of the present invention, said insertion, which is a duplication of 4 nucleotides (CCTG) normally found at position 1086-1089, is a 4 nucleotide insertion at the nucleotide position 1085 or 1090, an insertion of an adenosine at position 1284, or an insertion of a cytosine at position 1365 of the nucleotide sequence of Fig. 2A.

In another preferred embodiment of the invention, said deletion is a 13 nucleotide deletion of nucleotides 1085 -1097, a deletion of the thymidine at position 1051 or a deletion of the cytosine at position 1309 or 1313 of the nucleotide sequence of Fig. 2A .

In still another preferred embodiment of the present invention, said substitution is a cytosine to thymidine exchange at nucleotide position 889 a guanosine to thymidine exchange at nucleotide position 358, an adenosine to guanosine exchange at nucleotide position 374, a guanosine to adenosine exchange at nucleotide position 1052, or a cytosine to adenosine exchange at nucleotide position 1094 of the nucleotide sequence of Fig. 2A.

As mentioned above, said mutation results in a loss or a gain of function of the (poly)peptide of the invention. In a preferred embodiment of the present invention, said loss of function is a loss of macromolecule binding properties. However, a loss of transactivating property in addition or instead of the loss of the macromolecule binding property is also envisaged. Other possibilities relate to the loss of a structural determinant (truncated protein) in addition to the loss of a functional determinant.

For example, the experiments performed in accordance with the present invention suggest that at least some of the mutations identified so far in the AIRE gene lead to truncated forms of the (poly)peptide of the present invention lacking at least one of the PHD zinc fingers.

Based on the cellular localization studies performed in accordance with the present invention (for details see Examples 10 to 12) it is, furthermore, envisaged in accordance with the present

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invention, but without being bound to any scientific theory, that loss of function of the mutated/truncated (poly)peptides of the invention may be associated with their abnormal nuclear distribution. Thus, it is conceivable that the truncated (poly)peptides of the invention are erroneously directed to other nuclear structures by default as consequence of missing a domain normally interacting with either a core DNA target or chromatin-associated protein.

In addition, it could be shown in accordance with the present invention that AIRE interacts with structural components of the cytoplasmic compartment. More specifically, it is envisaged that AIRE associates with vimentin since AIRE harbors a cluster of basic amino acids within the nuclear targeting signal. Moreover, the apparently variable temporal and spatial decoration of filament arrays and nuclear speckles by anti-AIRE antibodies suggests the existence of a dynamic or passive trafficking of AIRE in the cell. Thus, it is also envisaged in accordance with the present invention that AIRE is residing on vimentin fibers as part of a docking mechanism regulating nuclear translocation. The occurrence of nuclear factors interacting with components of the cytoskeleton is not an unprecedented observation. An interesting example is the regulation of the function of *Gli* zinc finger transcription factor, vertebrate homologue of *Drosophila ci* gene (Biesecker, L.G. (1997). Strike three for GLI3 [news] [published erratum appears in Nat Genet 1998 Jan;18(1):88]. *Nature Genetics* 17, 259-260). This transcription factor is mainly targeted to the cytoplasm where it is anchored to microtubules, whereas a truncated form of Gli processed by proteolytic cleavage of the molecule is directed to the nucleus (Aza-Blanc, P., Ramirez-Weber, F.A., Laget, M.P., Schwartz, C. & Kornberg, T.B. (1997). Proteolysis that is inhibited by hedgehog targets Cubitus interruptus protein to the nucleus and converts it to a repressor. *Cell* 89, 1043-1053; Robbins, D.J., Nybakken, K.E., Kobayashi, R., Sisson, J.C., Bishop, J.M. & Therond, P.P. (1997). Hedgehog elicits signal transduction by means of a large complex containing the kinesin-related protein costal2. *Cell* 90, 225-234). To date, the only described nuclear factor interacting with vimentin is a protein component of the nuclear matrix, NMP125, transiently stored along vimentin during mitosis (Marugg, R.A. (1992). Transient storage of a nuclear matrix protein along intermediate-type filaments during mitosis: a novel function of cytoplasmic intermediate filaments. *Journal of Structural Biology* 108, 129-139). Thus, AIRE represents the first example of a zinc-finger protein co-localizing with vimentin intermediate filaments. With respect to the abnormal cytoplasmic localization, it is thus envisaged that loss of function may be associated with impaired protein-protein interactions involved in

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maintaining the shape and integrity of intermediate filaments. In other words, aggregates of the mutant (poly)peptides of the present invention may prevent the formation of vimentin intermediate filaments by, e.g., entrapping vimentin. On the other hand, it may also be envisaged that the above-mentioned docking/activation mechanism of the mutant (poly)peptides of the invention is impaired thereby leading to a loss of function.

Thus, the pathological consequences of at least some of the mutations found in the AIRE gene may elicit their effects at least in part by effecting the spatial organization of AIRE in the cell.

In an alternative preferred embodiment of the present invention, said gain of function is involved in molecular interaction. An example of such a gain of function is the indirect regulation of a cellular process. For instance, if the deletion of a zinc finger results in the loss of a binding property involving a second molecule, this second molecule may "gain" a function in case its function was modulated by APGD1.

The present invention further relates to a fragment of any of the aforementioned nucleic acid molecule(s) comprising at least 14 nucleotides. Preferably, said fragment is about 17 nucleotides long, and most preferably, it is about 21 nucleotides long. Said fragment can be used, e.g., as a probe in nucleic acid hybridization experiments like, e.g., Southern or Northern blot experiments, or as primer in primer extension analyses. In a preferred embodiment said fragment is labeled.

In another aspect, the present invention provides a nucleic acid molecule which is complementary to any of the nucleic acid molecules or fragments thereof described above. Such a nucleic acid molecule can be used, e.g., as a probe in RNase protection assays, or as an anti-sense probe to inhibit expression of the (poly)peptide(s) of the present invention. The person skilled in the art is familiar with the preparation and the use of said probes (see, e.g., Sambrook et al., supra).

In a further embodiment of the present invention, the nucleic acid molecule(s) of the invention are DNA molecules like, e.g., cDNA or genomic DNA molecules, or RNA molecules like mRNA molecules.

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In another embodiment, the present invention provides a primer pair which hybridizes under stringent conditions to any of the nucleic acid molecules mentioned above. Said primer pair can be used, e.g., in a polymerase chain reaction (PCR) to amplify nucleic acid fragments derived from the nucleic acid molecules described above. In the case that RNA is used as the template in the amplification reaction, it is beforehand reverse transcribed into DNA. The skilled artisan knows how to design and use said primer pair, which conditions for the amplification reaction have to be set up, and how to reverse transcribe RNA into DNA (see, e.g., Sambrook et al., *supra*).

Furthermore, the present invention relates to a vector comprising a nucleic acid molecule of the invention.

Examples for such vectors are, e.g., plasmids like, e.g., pUC18/19, pBR322 or pBlueScript all of which are commercially available. In addition, vectors of the present invention may be cosmids, viruses or bacteriophages used conventionally in genetic engineering that comprise the nucleic acid molecule of the invention. Preferably, said vector is a gene transfer or targeting vector. Such vectors may comprise further genes such as marker genes which allow for the selection of said vector in a suitable host cell and under suitable conditions. In another preferred embodiment the nucleic acid molecule present in the vector is operatively linked to regulatory elements permitting expression in prokaryotic or eukaryotic host cells. Expression of said polynucleotide comprises transcription of the polynucleotide into a translatable mRNA. Regulatory elements ensuring expression in eukaryotic cells, preferably mammalian cells, are well known to those skilled in the art. They usually comprise regulatory sequences ensuring initiation of transcription and, optionally, a poly-A signal ensuring termination of transcription and stabilization of the transcript, and/or an intron further enhancing expression of said polynucleotide. Additional regulatory elements may include transcriptional as well as translational enhancers, and/or naturally-associated or heterologous promoter regions. Possible regulatory elements permitting expression in prokaryotic host cells comprise, e.g., the PL, *lac*, *trp* or *tac* promoter in *E. coli*, and examples for regulatory elements permitting expression in eukaryotic host cells are the *AOXI* or *GALI* promoter in yeast or the CMV-, SV40-, RSV-promoter (Rous sarcoma virus), CMV-enhancer, SV40-enhancer or a globin intron in mammalian and other animal cells. Beside elements which are responsible for the

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initiation of transcription such regulatory elements may also comprise transcription termination signals, such as the SV40-poly-A site or the tk-poly-A site, downstream of the nucleic acid molecule of the invention. Furthermore, depending on the expression system used leader sequences capable of directing the polypeptide to a cellular compartment or secreting it into the medium may be added to the coding sequence of the polynucleotide of the invention and are well known in the art. The leader sequence(s) is (are) assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein, or a portion thereof, into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an C- or N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pCDM8, pRc/CMV, pcDNA1, pcDNA3 (In-vitrogene), pSPORT1 (GIBCO BRL)) or pCI (Promega).

Preferably, the expression control sequences will be eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells, but control sequences for prokaryotic hosts may also be used.

As mentioned above, the vector of the present invention may also be a gene transfer or targeting vector. Gene therapy, which is based on introducing therapeutic genes into cells by ex-vivo or in-vivo techniques is one of the most important applications of gene transfer. Suitable vectors and methods for in-vitro or in-vivo gene therapy are described in the literature and are known to the person skilled in the art; see, e.g., Giordano, Nature Medicine 2 (1996), 534-539; Schaper, Circ. Res. 79 (1996), 911-919; Anderson, Science 256 (1992), 808-813; Isner, Lancet 348 (1996), 370-374; Muhlhauser, Circ. Res. 77 (1995), 1077-1086; Wang, Nature Medicine 2 (1996), 714-716; WO94/29469; WO 97/00957 or Schaper, Current Opinion in Biotechnology 7 (1996), 635-640, and references cited therein. The polynucleotides and vectors of the invention may be designed for direct introduction or for introduction via liposomes, or viral vectors (e.g. adenoviral, retroviral) into the cell. Preferably, said cell is a germ line cell, embryonic cell, or egg cell or derived therefrom, most preferably said cell is a stem cell.

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The invention also relates to a host comprising a vector according to the invention. The transformation of hosts with the vectors of the invention is well known in the art (see, e.g., Sambrook et al., *supra*).

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adeno-associated virus, herpes viruses, or bovine papilloma virus, may be used for delivery of the polynucleotides or vector of the invention into targeted cell population. Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors; see, for example, the techniques described in Sambrook et al., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory (1989) N.Y. and Ausubel et al., *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y. (1989). Alternatively, the polynucleotides and vectors of the invention can be reconstituted into liposomes for delivery to target cells. The vectors containing the polynucleotides of the invention can be transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas, e.g., calcium phosphate or DEAE-Dextran mediated transfection or electroporation may be used for other cellular hosts; see Sambrook, *supra*.

In a preferred embodiment of the present invention, the host is a bacterium, a yeast cell, an insect cell, a fungal cell, a mammalian cell, a plant cell, a transgenic animal or a transgenic plant. As used herein, the term "transgenic" also relates to organisms that contain a gene which has been knocked out. For example, animals with no functional allele of the APGD1-gene can be used for the investigation of the role APGD-1 plays in cellular life as well as a model for the development of APECED. Techniques for the production of transgenic or knock-out organisms are well known in the art.

In a further embodiment, the present invention relates to a process of producing a (poly)peptide of the invention comprising culturing or raising the host described above and isolating said (poly)peptide from said culture or said host. Such methods are well known in the art (see, e.g., Sambrook et al., *supra*).

Furthermore, the invention relates to a (poly)peptide encoded by a nucleic acid molecule of the invention or produced by the above described process. In this context it is also understood

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that the (poly)peptides according to the invention may be further modified by conventional methods known in the art. By providing the (poly)peptides according to the present invention it is also possible to determine the portions relevant for their biological activity. This may allow the construction of chimeric proteins or fusion proteins comprising an amino acid sequence derived from a (poly)peptide of the invention which is crucial for its biological activity and other functional amino acid sequences like, e.g., nuclear localization signals, transactivating domains, DNA-binding domains, hormone-binding domains, protein tags (GST, GFP, h-myc peptide, Flag, HA peptide) which may be derived from the same or from heterologous proteins. Said chimeric or fusion proteins are also comprised by the present invention.

The present invention also relates to a compound derived from a (poly)peptide of the invention and having essentially the same three dimensional structure thereof. Said compounds can be theoretically constructed on computers using molecular modelling software and subsequently be synthesized. Since such compounds are preferably not of proteinaceous nature, they may be used in applications where proteolytic degradation should be avoided, e.g., when contained in pharmaceutical compositions that are applied orally. The design of such compounds may, e.g., be effected by peptidomimetics.

In a further embodiment, the present invention relates to an antibody that specifically recognizes the (poly)peptide of the invention. Namely, the invention relates to an antibody which specifically recognizes (poly)peptides according to the invention irrespective of whether they are the wild-type or a mutated form and/or depending on whether the (poly)peptide of the invention is the wild-type or a mutated form. The antibody of the present invention may be a monoclonal antibody, a polyclonal antibody or a synthetic antibody as well as a fragment of said antibodies, such as, e.g., a Fab, a Fv or a scFv fragment. Furthermore, the antibody or fragments thereof can be obtained by using methods which are described, e.g., in Harlow and Lane, "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. The antibody of the present invention can be used, e.g., for the immunoprecipitation and immunolocalization of the (poly)peptides of the invention as well as for the monitoring of the presence of such (poly)peptides, e.g., in recombinant organisms, and for the identification of compounds interacting with the (poly)peptides according to the invention.

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Moreover, the present invention relates to a pharmaceutical composition comprising at least one of the aforementioned nucleic acid molecules, vectors, (poly)peptides, three-dimensionally equivalent compounds, and/or the antibody according to the present invention either alone or in combination, and optionally a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions etc. Compositions comprising such carriers can be formulated by conventional methods. The pharmaceutical compositions can be administered to the subject at a suitable dose. Administration of the suitable compositions may be effected by different ways, e.g. by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. The dosage regimen will be determined by the attending physician and other clinical factors. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Generally, the regimen as a regular administration of the pharmaceutical composition should preferably be in the range of 1 μ g to 10 mg units per day. If the regimen is a continuous infusion, it should preferably also be in the range of 1 μ g to 10 mg units per kilogram of body weight per minute, respectively. Progress can be monitored by periodic assessment. Dosages will vary but a preferred dosage for intravenous administration of DNA is preferably from approximately 10^6 to 10^{22} copies of the DNA molecule. The compositions of the invention may be administered locally or systemically. Administration will generally be parenterally, e.g., intravenously; DNA may also be administered directly to the target site, e.g., by biolistic delivery to an internal or external target site or by catheter to a site in an artery.

In addition, the present invention relates to a diagnostic composition comprising at least one of the aforementioned nucleic acid molecules, vectors, (poly)peptides, three-dimensionally equivalent compounds, and/or the antibody according to the present invention either alone or in combination.

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Said diagnostic composition can be used to test for a carriership for APECED or for a corresponding disease state comprising testing a sample obtained from a prospective patient or from a person suspected of carrying a predisposition for a mutation in the nucleic acid molecule(s) of the invention. Furthermore, the diagnostic composition can be used to test for a carriership for APECED or for a corresponding disease state comprising testing a sample obtained from a prospective patient or from a person suspected of carrying a predisposition for a mutated form of the (poly)peptide(s) according to the invention in an immuno-assay using the antibody of the invention. The term "immuno-assay", as used herein, comprises methods like, e.g., immuno-precipitation, immuno-blotting, ELISA, RIA, indirect immuno-fluorescence experiments, and the like. Such techniques are well known in the art and are described, e.g. in Harlow and Lane, *supra*.

The components of the composition of the invention may be packaged in containers such as vials, optionally in buffers and/or solutions. If appropriate, one or more of said components may be packaged in one and the same container.

In another embodiment, the present invention relates to methods for testing for a carriership for APECED or for a corresponding disease state comprising testing a sample obtained from a prospective patient or from a person suspected of carrying a predisposition for a mutation in the nucleic acid molecule(s) of the invention. Such methods comprise, e.g., Southern blotting or amplifying nucleic acid molecules from a nucleic acid obtained from a prospective patient or from a person suspected of carrying a predisposition for APECED with the primer pair of the invention, and analyzing the amplified nucleic acid molecules for the presence of a mutation. Said nucleic acid molecules can be analyzed, e.g., by sequencing with the primer or probe of the invention, hybridizing with the primer of the invention or by size-fractionating said nucleic acid molecules by gel-electrophoresis. Alternatively, and by way of example said nucleic acid obtained from a prospective patient or from a person suspected of carrying a predisposition for APECED can be directly analyzed by sequencing or hybridizing with the primer or probe of the invention. All the above mentioned primers or probes may hybridize to a mutated or a wild-type sequence. Further, all of the aforescribed methods are well known in the art (see, e.g., Sambrook et al., *supra*).

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In yet another embodiment, the present invention relates to methods for testing for a carriership for APECED or for a corresponding disease state comprising testing a sample obtained from a prospective patient or from a person suspected of carrying a predisposition for a mutated form of the (poly)peptide(s) according to the invention. Such methods comprise, e.g., immuno-precipitation, immuno-blotting, ELISA, RIA, indirect immuno-fluorescence experiments, and the like. Such techniques are well known in the art and are described, e.g. in Harlow and Lane, *supra*.

In another embodiment, the present invention relates to the use of the nucleic acid molecule(s) or the vectors of the invention for gene therapy. Vectors comprising a nucleic acid molecule of the invention may be stably integrated into the genome of the cell or may be maintained in an extrachromosomal form. On the other hand, viral vectors described in the prior art may be used for transfecting certain cells, tissues or organs. Suitable gene delivery systems may include liposomes, receptor-mediated delivery systems, naked DNA, and viral vectors such as herpes viruses, retroviruses, adenoviruses, and adeno-associated viruses, among others. Delivery of nucleic acid molecules to a specific site in the body for gene therapy may also be accomplished using biolistic delivery systems.

Standard methods for transfecting cells with nucleic acid molecules are well known to those skilled in the art, see, e.g., Sambrook et al., *supra*. Gene therapy to cure APECED may be carried out by directly administering the nucleic acid molecule of the invention encoding a functional form of APGD1 to a patient or by transfecting cells with said nucleic acid molecule of the invention *ex vivo* and infusing the transfected cells into the patient. Furthermore, research pertaining to gene transfer into cells of the germ line is one of the fastest growing fields in reproductive biology. Gene therapy, which is based on introducing therapeutic genes into cells by *ex-vivo* or *in-vivo* techniques is one of the most important applications of gene transfer. Suitable vectors and methods for *in-vitro* or *in-vivo* gene therapy are described in the literature and are known to the person skilled in the art. The nucleic acid molecules comprised in the pharmaceutical composition of the invention may be designed for direct introduction or for introduction via liposomes, or viral vectors (e.g. adenoviral, retroviral) containing said nucleic acid molecule into the cell. Preferably, said cell is a germ line cell, embryonic cell, or

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egg cell or a cell derived therefrom, if the production of transgenic non-human animals is envisaged.

It is to be understood that the introduced nucleic acid molecule encoding the protein having the biological activity of APGD1 expresses said protein after introduction into said cell and preferably remains in this status during the lifetime of said cell. For example, cell lines which stably express said protein having the biological activity of APGD1 may be engineered according to methods well known to those skilled in the art. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with the recombinant DNA molecule or vector of the invention and a selectable marker, either on the same or separate vectors. Following the introduction of foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows for the selection of cells having stably integrated the plasmid into their chromosomes and growing to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the protein having the biological activity of APGD1. A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase, and adenine phosphoribosyl-transferase in tk, hgp^{rt} or ap^{rt} cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate, gpt, which confers resistance to mycophenolic acid, neo, which confers resistance to the aminoglycoside G-418, hyg^{ro}, which confers resistance to hygromycin, or puromycin (pat, puromycin N-acetyl transferase). Additional selectable genes have been described, for example, trp^B, which allows cells to utilize indole in place of tryptophan; his^D, which allows cells to utilize histinol in place of histidine, and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO.

The documents cited in the present specification are herewith incorporated by reference.

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The figures show:

Figure 1

A) The physical map of the APECED region showing the markers used to construct the disease haplotypes (cen - JA1, D21S1912, PFKL (CA_n), PB1, D21S171 - tel), the other genes (PFKL, green and 694N10, pink) and the ESTs (EST cluster 1: AA082879, AA085392, EST cluster 2: N67176, T84071, T86112, T79577, T79655, R23544, R44295, EST cluster 3: AA453553) located in the close vicinity of APGD1 (blue) and the key cosmid clones Q21D11 and Q22G11 used for genomic sequencing as well as cosmid clone Q11D11 that was used as orientation marker in the fiber FISH experiment (see Figure 1C).

B) The genomic structure of the APGD1 gene. The 14 true exons of the gene are compared with the gene models predicted with different gene finding programs (Uberbacher, E., et al., *Proc. Natl. Acad. Sci. USA*, **88**, 11261-11265 (1991); Thomas, A., & Skolnick, M. H., *IMA J. Math. Appl. Med. Biol.*, **11**, 149-160 (1994); Kulp, D., et al., ISMB-96, St. Louis, MO, AAAI/MIT Press. (<http://www-hgc.lbl.gov/projects/genie.html>) (1996)). Solid boxes indicate exons in which at least one boundary was correctly predicted, open boxes are false exons. Genomic sequence of cosmid clones Q21D1, Q22G11, EST matches, detailed gene prediction data and the intron-exon boundaries of APGD1 are available at <http://chr21.rz-berlin.mpg.de/APECED.html/>.

C) Fiber FISH image showing the assignment of the APGD1, red signal, (cDNA clone B1-1 used as a probe) in relation to previously mapped cosmid clones, Q11D11 (yellow) and Q21D1 (green). Detailed protocol is described elsewhere (Heiskanen, M., et al., *TIG*, **10**, 379-382 (1996)).

Figure 2

A) The nucleotide and predicted amino acid sequence of human APGD1. The boundaries corresponding to the composite cDNA sequence are indicated by brackets, the most 3' end nucleotides for cDNA clones B1-1 and D1-1 are at positions 1809 and 2181, respectively. The last 64 nucleotides were determined by PCR extension. A putative non-canonical polyadenylation signal was found at nucleotide 2191 (underlined). The Alu sequence overlapping with the PFKL promotor is starting at nucleotide 1995 (arrowed bracket). Silent

polymorphisms are indicated by small arrows (nucleotides 708, 801, 1317 and 1698). The predicted protein is 545 amino acids. The putative bi-partite nuclear localisation signal is underlined in blue. The two PHD zinc finger domains are underlined in magenta. The cDNA sequence has been deposited in EMBL (Accession No. Z97990).

B) Northern blot analysis using cDNA B1-1 (1,8 kb) as a probe on a multiple tissue Northern blot, each lane containing 2 µg poly(A) RNA from human adult tissues (Clontech catalog # 7754-1 and 7751-1). The lower panel shows the hybridization with the β-globin control probe.

Figure 3

The mutations in the APGD1 gene (see also Table 1). A) The C-lanes of the sequencing gel showing a patient homozygous for the Finnish major mutation and a normal control. C₈₈₉ of the patient has been mutated to T. B) A-lanes of a normal control and a Finnish patient heterozygous for the haplotype 4.1 show an A insertion at position 1284. C) Homozygous deletion of C₁₃₁₃ is observed in C-lane of the sequence of a French patient also homozygous for the disease haplotype 5.1. D) Comparison of C-lanes of an Italian patient homozygous for the haplotype 2.1 and normal control reveal a 4 bp insertion (nucleotides 1086-1089). E) A 13 bp deletion (nucleotides 1085-1097) can be observed in C-lanes of a patient carrying haplotype 3.1 compared with a normal control.

Figure 4

Schematic diagram of the AIRE constructs. The full length protein is 545 amino acids. Gray boxes indicate the PHD zinc finger domains, the hatched box the nuclear localization signal. The AIRE-ΔSacI mutant is truncated after 306 amino acids, the AIRE-ΔBamHI mutant after 209 amino acids.

Figure 5

Western blot analysis of cell extracts from transiently transfected COS1 cells. Cells were transfected with the indicated plasmids. The blot was probed with sp97181 antiserum. Expression of the full length protein (lanes 3 and 4) is compared with Mock (lane 1) or pSG5-only transfected cells (lane 2). Expression of the mutant proteins is shown in lane 5 (AIRE-ΔSacI) and lane 6 (AIRE-ΔBamHI). Arrows indicate the detected proteins for AIRE, AIRE-ΔSacI and AIRE-ΔBamHI constructs.

Figure 6

Subcellular distribution of the AIRE protein. COS1 cells were transfected with 5 μ g pSG5-AIRE and stained for AIRE with antibody sp97181 (red) after 24 h. Nuclei were stained with YOYO-1 (green). Images were scanned using a confocal laser microscope scanner. (I) Nuclear localization; Nu: Nucleoli. (II) Cytoplasmic and nuclear localization of AIRE. (a) Red and green images merged; overlapping signals appear yellow. (b) Red image. (c) Green image.

Figure 7

Co-localization of cytoplasmic AIRE with vimentin. COS7 cells (I and II) or human primary fibroblasts (III) were transfected with pSG5-AIRE and co-stained for AIRE (sp97181, red) and vimentin (green) after 24 h (I and II) or 48 h (III). Images were analyzed with an epifluorescence microscope. (a) Red and green images merged; co-localization of AIRE with vimentin appears yellow. (b) Red image. (c) Green image.

Figure 8

AIRE- Δ SacI forms nuclear inclusions and co-localizes with vimentin in COS7 cells. COS7 cells were transfected with pSG5-AIRE- Δ SacI and co-stained for AIRE (sp97181, red) and vimentin (green) after 24 h (I) or 48 h (II and III). Nuclei were stained with DAPI (blue, I and III). (a) Red, green and blue images merged. Co-localization of AIRE- Δ SacI and vimentin appears yellow. (b) Red image. (c) Green image. White arrowheads indicate nuclear AIRE- Δ SacI.

Figure 9

Subcellular localization of AIRE- Δ SacI and co-localization with vimentin in human primary fibroblasts. Fibroblasts were transfected with pSG5-AIRE- Δ SacI and co-stained for AIRE (sp97181, red) and vimentin (green) after 48 h. (I) Nuclear localization of AIRE- Δ SacI, (II) cytoplasmic co-localization of AIRE- Δ SacI with vimentin. (a) Red and green images merged; co-localization of AIRE with vimentin appears yellow. (b) Red image. (c) Green image. White arrowheads indicate nuclear AIRE- Δ SacI.

Figure 10

AIRE- Δ BamHI forms cytoplasmic aggregates and nuclear inclusions in COS7 cells. COS7 cells were transfected with pSG5-AIRE- Δ BamHI and stained for AIRE (sp97181, red) after 24 h (II) or 48 h (I and III) and vimentin (green, II and III). Nuclei were stained with DAPI (blue, I and II). (a) Images merged; co-localization of AIRE with vimentin appears yellow. (b) Red image. (c) Green image. White arrowheads indicate nuclear AIRE- Δ BamHI.

Figure 11

Subcellular localization of AIRE- Δ BamHI and co-localization with vimentin in human primary fibroblasts. Fibroblasts were transfected with pSG5-AIRE- Δ BamHI and co-stained for AIRE (sp97181, red) and vimentin (green) after 48 h. Nuclei were stained with DAPI (blue). (I) Cytoplasmic aggregates and nuclear AIRE- Δ BamHI. (II) Cytoplasmic filamentous localization of AIRE- Δ BamHI. (a) Images merged; co-localization of AIRE with vimentin appears yellow. (b) Red image. (c) Green image. White arrowheads indicate nuclear AIRE- Δ BamHI.

Figure 12

Genomic structure of the mouse and human AIRE gene showing the positions of the fourteen exons, the position of the TATA box and a conserved region 3 kb upstream of the first exon. CpG islands and repetitive elements are depicted as solid boxes and arrows, respectively (B1, B1-F, PB1D9=Alu-like repeats in mouse; B2, B4, MIR=various short interspersed nucleotide elements; L1, L2=various long interspersed nucleotide elements; LTR=long terminal repeats; MER = DNA transposon elements). The human AIRE gene locus (cosmid Q22G11) was previously sequenced.

Figure 13

Dot-matrix of sequence comparison of the human and murine AIRE gene structure (A). Arrows mark exons. Arrowhead denotes conserved region shown in detail in Figure 13B.

Figure 14 .

cDNA sequence of murine AIRE gene and deduced amino acid sequence.

Figure 15

The murine AIRE gene is located on chromosome 10. PCR amplification of monochromosomal mouse hybrids, using mouse specific primers Mforw2 Mrev32 (see Example 16). M is 100 bp ladder marker; 1: hybrid containing mouse chr. 10; 2: hybrid containing mouse chr. 3; 3: hybrid containing mouse chr. 3+17, 4: total mouse genomic DNA; 5: total human genomic DNA; 6: water negative control.

Figure 16

Amino acid sequence comparison of the human and murine AIRE protein. Shaded boxes mark PHD fingers and the dotted line the SAND domain. The nuclear localization signal (NLS) is underlined, and the LXXLL-motif is boxed.

Figure 17

Differential splicing of the mouse AIRE gene. Amino acid sequence is indicated above the nucleic acid sequence.

- (a) Shows skipping of exon 10;
- (b) Shows deletion of a lysine in exon 8;
- (c) Shows deletion of Proline, Isoleucine, Threonine, Valine in exon 6.

Figure 18

Expression of human in a series of immunological tissues. RT-PCR amplification was performed as described in Example 15. Lanes 1 to 8 correspond to: fetal liver, lymph node, peripheral blood leukocyte, thymus, bone marrow and spleen respectively. Lane 9 is negative control; M1 is lambda HindIII marker, M2 is 100 bp ladder marker.

The examples illustrate the invention

Example 1: Isolation of the human APGD1-cDNA

We have mapped APECED to chromosome 21q22.3 by linkage analysis and further refined the localisation by linkage disequilibrium to a region between the markers D21S25 and D21S171

(Aaltonen, J., et al., *Nature Genet.*, **8**, 83-87 (1994); Aaltonen et al., *Genome Research* **7** (1997), 820-827). This critical region was 350 kb in size and a bacterial clone contig was constructed across this region. Several techniques were used to identify candidate genes in this gene rich region. Exon trapping (Buckler, A., et al., *Proc. Natl. Acad. Sci., USA*, **88**, 4005-4009, (1991)) and cDNA selection (Lovett, M., et al., *Proc. Natl. Acad. Sci., USA*, **88**, 9628-9632, (1991)) methods identified a new gene, 694N10 (Accession No. Z93322), just distal to the previously known PFKL gene (Phosphofructokinase of liver type, EC 2.7.1.11) (Elson et al., *Genomics*, **7**, 47-56 (1990)) (Figure 1A). Partial unordered genomic sequence encompassing the PFKL gene (available at the International Chromosome 21 genomic sequence repository, <http://www-eri.uchsc.edu/chr21/eridna.html>) was used to generate a new polymorphic marker, PB1. This marker showed an obligatory recombination in one APECED family, thus we were able to restrict the APECED region to 145 kb between the markers D21S25 and PB1 (Figure 1A). Therefore 694N10 was excluded as causative gene for APECED.

In parallel, we initiated a large scale sequencing approach from cosmid clones 21D1 and 22G11 mapping to the critical region (Figure 1A). A total of 87 kb of genomic sequence obtained from these cosmids were analysed with BlastN and BlastX algorithms (Altschul, S. F., et al., *J. Mol. Biol.*, **215**, 403-410, (1990)) against public databases. Three different EST (Expressed Sequence Tag) clusters were found in a region between D21S25 and PFKL (Figure 1A). Exon prediction was performed using the GRAIL2 program (Uberbacher, E., et al., *Proc. Natl. Acad. Sci., USA*, **88**, 11261-11265 (1991)). A gene model was predicted directly upstream of the promotor of PFKL where no EST matches were identified (exons G1 to G7, Figure 1B). However, since the linkage disequilibrium data (Björnses, P., et al., *Am. J. Hum. Genet.*, **59**, 8779-886 (1996)) suggested the APECED gene to be located in the close vicinity of PFKL further analyses were focused on this potential gene. Polymerase Chain Reaction (PCR) amplification (5'-AGA AGT GCA TCC AGG TTG GC-3' and 5'-GGA AGA GGG GCG TCA GCA AT-3') of a 316 bp genomic fragment spanning predicted exons G5 and G6 (Figure 1B) generated a probe for screening a human adult thymus cDNA library (Clontech catalog # HL5010b). Two cDNA clones (B1-1 and D1-1) and a 3' UTR extension PCR product yielded a composite cDNA sequence of 2,245 kb (Figure 2A). The cDNA clone B1-1 was localised on the physical map by fiber FISH (Fluorescent In Situ Hybridization) (Figure 1C) (Heiskanen, M., et al., *TIG*, **10**, 379-382 (1996)). Northern blot analysis showed a major transcript of approximately 2 kb expressed

in all tissues analysed, the most intensive signals were obtained from thymus, pancreas and adrenal cortex (Figure 2B). In this respect, it is surprising that no ESTs were found in the databases. The cDNA sequence exhibits an unusually high GC content of 68.8% and contains an open reading frame (ORF) of 581 amino acids followed by a STOP codon at nucleotide 1756. The likely initiator ATG codon occurs at nucleotide 121 (Figure 2A), predicting a 545 residue protein.

Example 2: Structure of the APGD1-gene

The structure of the APGD1 gene was determined from a comparison of the cDNA sequence with the cosmid 22G11 genomic sequence using the est_genome program (developed by Richard Mott, available at the Sanger center, UK). The genomic structure consists of 14 exons spanning 11,9 kb of genomic DNA (Figure 1B). A putative promotor containing a TATA box located 35 nucleotides from the first nucleotide of exon 1 and a GC box was identified immediately upstream of the first exon of the APGD1 gene. A CpG island was also associated with the promotor region. Detailed analysis of the genomic sequence upstream of the APGD1 gene did not suggest any additional exons within 22 kb of the predicted promotor. The translation of the genomic sequence identified an in frame STOP codon 16 residues upstream of the first amino acid of the translated cDNA sequence. Analysis of the 3' end of the gene suggested that exon 14 represents the last exon since the STOP codon at position 1756 is followed by repetitive sequences. Further, exon 14 overlaps with the promoter region of the PFKL gene (Levanon, D., et al., *Biochem and Mol. Biol. Int.*, 35, 929-936 (1995)) which is transcribed from the same DNA strand (Figure 1B and 2A). Apparent C to T silent polymorphisms were found at third codon positions in exons 5, 6, 10 and 14 (Figure 2A). The gene organisation was poorly predicted by GRAIL: only three (exons 2, 4 and 6) of the 14 exons were identified *bona fide* and 7 exons were completely missed (Figure 1B). Yet, the gene is located in a GC rich region and intron-exon boundaries follow the GT-AG rule (Mount, S.M., et al., *Nucleic Acids Research.*, 10, 459-472 (1982)). Subsequent analysis of the genomic sequence with other gene finding software including GRAIL1a (Uberbacher, E., et al., *Proc. Natl. Acad. Sci. USA*, 88, 11261-11265 (1991)), Xpound (Thomas, A., & Skolnick, M. H., *IMA J. Math. Appl. Med. Biol.*, 11, 149-160 (1994)), and Genie (Kulp, D., et al., ISMB-96, St. Louis, MO, AAAI/MIT Press. (<http://www-hgc.lbl.gov/projects/genie.html>) (1996)) showed

that Genie, based on hidden Markov model, performed best for modeling the 3' end of this gene (Figure 1B).

Example 3: APECED-associated mutations found in the APGD1-gene

For mutation screening in APECED patients, all 14 exons were amplified from genomic DNA using primers located in the respective flanking introns (primer sequences and the detailed protocols available at <http://chr21.rz-berlin.mpg.de/APECED.html>). Five different mutations were identified in the coding region of APGD1 (Table 1). The mutations were monitored in a control panel of 500 unrelated Finns and 60 unrelated Europeans including 32 CEPH parents. The most common mutation was the "Finnish major mutation" found in 82% of the Finnish patients, all of which have the major disease haplotype (No. 1.1 in Table 1) (Björnses, P., et al., *Am. J. Hum. Genet.*, **59**, 8779-886 (1996)). This mutation is a C to T transition at nucleotide 889 in exon 6, changing an Arg into a STOP codon. Among the 500 Finns this mutation was detected in two heterozygotes, indicating a carrier frequency of 1: 250. The same mutation was also found in an Italian and in a German patient, who carried different haplotypes (haplotypes No. 1.2 to 1.4 in Table 1, respectively). Two mutations were found in exon 8. The first one is a duplication of four nucleotides (CCTG) normally found at position 1086 to 1089. The other mutation in this exon is a 13 bp deletion (nucleotides 1085 to 1097) observed in four non-Finnish patients (two British, a Dutch and a German) carrying the same haplotype (No. 2.1 in Table 1). Two other mutations which involve insertion or deletion of a single nucleotide were found in exon 10. The insertion of an A at position 1284 was found in two compound heterozygote Finnish patients having the Finnish major mutation in the other allele. Deletion of a C was found at position 1313 in a French patient homozygous for the disease haplotype (No. 5.1 in Table 1). Mutations and the associated haplotypes are summarized in Figure 3 and Table 1. Northern blot analysis performed on lymphoblast mRNA from patients whose cell lines were available (all Finnish patients) did not show a size difference of the transcript or altered level of expression when compared to control subjects. All the mutations cosegregated with the disease in the respective families and were predicted to result in truncation of the conceptual protein (Table 1). This provides strong evidence that alterations of the APGD1 gene represent the primary cause for the APECED disease.

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Example 4: Recombinant AIRE expression in *E. coli* and purification of the protein

The QIA expressionist method (Qiagen) was used for bacterial expression and purification of the 6x His-tagged recombinant AIRE protein. A 1.8 kb *SalI/NotI* cDNA fragment derived from clone B1-1pA () and containing the complete AIRE coding sequence was cloned into the pQE32N vector (pQE32N-AIRE). The correct cloning orientation and the reading frame were verified by sequencing. *E. coli* strain SCS1 pSE III was transformed with pQE32N-AIRE and protein expression was induced for 4 h with 1 mM isopropyl-b-thiogalactopyranoside (IPTG). The His-tagged protein was purified under denaturing conditions on a Ni-NTA Agarose column according to the manufacturer's recommendations (Qiagen), and analyzed by SDS-PAGE and Western Blotting.

Example 5: AIRE expression plasmids for transient transfection

For expression of the full length 545 amino acids protein in mammalian cells the 1.8 kb *EcoRI* insert from B1-1pA AIRE cDNA was cloned into the expression vector pSG5 (Invitrogen) and named pSG5-AIRE. The correct orientation was verified by restriction digest and sequencing. AIRE deletion mutants were generated by restriction digests using unique restriction sites in the cDNA. The pSG5-AIRE- Δ BamHI construct was generated by deleting a 1.1 kb *Bam*HI 3'-terminal fragment from pSG5-AIRE cDNA, producing a protein that is truncated at residue 209. In this construct, a stop codon is provided by the pSG5 vector sequence after encoding for 17 nonsense amino acids at the AIRE- Δ BamHI C-terminus. The pSG5-AIRE- Δ SacI construct was generated by deleting a 0.8 kb *SacI/BglII* fragment from pSG5-AIRE cDNA and religation of the DNA molecule after generating blunt ends by T4 DNA polymerase and Klenow Fragment. This construct encodes for a protein truncated at amino acid 306; a stop codon is provided by the vector sequence after encoding for 2 nonsense amino acids at the C-terminus of AIRE- Δ SacI.

Example 6: Antibody production and purification

Polyclonal antibodies against the AIRE protein were obtained by injecting rabbits with the synthetic peptides MATDAALRRLRLHR (corresponding to aa 1-15) and

SQPRKGRKPPAVPK (corresponding to aa 107-120), respectively. The resulting immune sera sp97179 (for aa 1-15) and sp97181 (for aa 107-120) were affinity purified against their corresponding synthetic peptides immobilized on a HiTrap NHS-activated 1 ml column (Pharmacia) according to the manufacturer's recommendations.

Example 7: Cell culture and transfection experiments

COS 1 cells were maintained at 37°C and 5% CO₂ in Dulbecco's Modified Eagle Medium (DMEM) containing 1000 mg/l glucose, 10% Fetal Calf Serum, 10 U/ml Penicillin and 10 µg/ml Streptomycin. Transfections were performed by electroporation as follows: 10⁶ cells grown at 80-90% confluence were centrifuged, washed twice in ice-cold phosphate buffered saline (PBS) containing 2 mM Hepes (HeBS) and resuspended in 800 µl HeBS. DNA was diluted in 130 µl HeBS before being added to the cells (either 2, 5, 10 or 20 µg of DNA). After 10 min incubation on ice, cells were pulsed with a field strength of 3 kV/cm (capacitance 25 µf) using a Gene Pulser (Bio-Rad). Cells were allowed to recover on ice for 10 min before being transferred in 10 ml pre-equilibrated DMEM containing 25 mM Hepes. Transfected cells were seeded in Leighton tubes (Costar) for immunofluorescence studies (1.5x10⁵ cells / Leighton) and in 10 cm petri dishes (4x10⁵ cells/dish) for cell extract preparations and incubated at 37°C and 5% CO₂ for 24 h or 48 h. COS7 cells and fibroblasts were maintained at 37°C and 5% CO₂ in DMEM/F12 medium containing 1000 mg/l glucose, 10 % Fetal Calf Serum, 10 U/ml Penicillin and 10 µg/ml Streptomycin. Cells were transfected using the LipofectACE method according to the manufacturer's recommendations (Gibco Life Technologies). Cells were seeded into a six-well-plate containing glass cover slips (4x10⁵ cells per well) and allowed to grow for 24 h before transfection. Transfections were performed using 3 µg of DNA per well and cells were incubated in the LipofectACE/DNA mix for 6 h. Cells were analyzed by indirect immunofluorescence 48 h post-transfection.

Example 8: Indirect Immunofluorescence

Cells were fixed either with methanol/acetone or paraformaldehyde (PFA).

Methanol/acetone fixation: Cells were briefly rinsed in PBS, fixed in 1:1 methanol/acetone for 10 min at -20°C, air dried and then incubated at 4°C overnight in PBS containing 3% Bovine

Serum Albumin (BSA). After a brief rinse in PBS, cells were incubated with antisera sp97179 or sp97181 diluted 1:200 in PBS/0.1% Triton X-100 (PBS-T) for 1 h at room temperature. Cells were washed three times in PBS-T for 10 min followed by 1 h incubation with a Cy3 labeled anti-rabbit antibody (Jackson Immuno Research) diluted 1:200 in PBS. Cells were washed twice in PBS-T and once in PBS for 10 min before staining with 12 nM YOYO-1 iodide in PBS (Molecular Probes) for 15 min. After washing in PBS three times for 5 min, preparations were mounted in 75% glycerol/ PBS.

PFA-fixation: Cells were briefly rinsed in PBS before fixation in 3.7% PFA in PBS for 10 min at room temperature. Cells were again briefly rinsed and then permeabilized with PBS/0.2% Triton X-100 for 10 min. Blocking and incubation with the AIRE antibodies were performed as described above, except that blocking was reduced to 1 h at room temperature.

Simultaneous detection of AIRE and vimentin was performed by co-staining cells with sp97179 (or sp97181) and anti-vimentin-antibodies. Vimentin polyclonal antibody raised in goat (produced by standard techniques well known to the person skilled in the art) was diluted 1:400 and incubated for 1 h, followed by incubation with a FITC-conjugated donkey-anti-goat secondary antibody (Jackson Immuno Research) diluted 1:200 in PBS. Coverslips were mounted in Vectashield (Vector Laboratories) containing 5 µg/ml DAPI.

Cells were either visualized and scanned with a confocal laser microscope (LSM 510-axioplan2, Zeiss) or analyzed with an epifluorescence microscope (Axioskop 50, Zeiss). Photos were taken with a CCD camera.

Example 9: Western Blot Analysis

Harvested cells were lysed in a buffer containing: 2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris pH 8, 1 mM EDTA and supplemented with 2 mM PMSF, 10 mM b-mercaptoethanol, 10 µg/ml Leupeptin and 10 µg/ml Pepstatin. 20 µg of total protein extracts were separated by 12% SDS-PAGE and blotted on a PVDF membrane. The membrane was blocked for 2 h in TBS-T (20 mM Tris pH 7.5, 150 mM NaCl, 0.05% Tween-20) containing 3% BSA followed by incubation with the polyclonal antiserum (sp97179, sp97181) diluted 1:1000 in TBS-T for 1 h. After washing the membrane three times for 5 min in TBS-T, the membrane was incubated for 1 h with an anti-rabbit IgG alkaline phosphatase conjugate (Calbiochem) diluted 1:5000 in PBS-T. The membrane was then washed three times for 5 min

in TBS-T, briefly rinsed twice in TBS and incubated in Western Blue Stabilized Substrate (Promega) for 6 min. The reaction was stopped by rinsing the membrane with H₂O.

In order to demonstrate the specificity of the antibodies in immunofluorescence and Western blot detection, experiments were repeated after pre-incubation of the antisera with an excess of His-tagged AIRE recombinant protein in PBS-T for 1 h at room temperature.

Example 10: Transient Expression of AIRE and Characterization of Polyclonal Antibodies

In order to investigate the cellular sub-localization of wild-type and deletion mutants of the AIRE protein in mammalian cells, the constructs shown in Figure 4 were designed. The full-length construct contains a cDNA encoding for the 545 residues AIRE protein (AIRE-B1-1pA). Two AIRE mutants truncated at amino acid residues no. 306 and no. 209 were designated AIRE-Δ SacI and AIRE-ΔBamHI, respectively. AIRE-ΔSacI is truncated within PHD1, whereas AIRE-ΔBamHI is lacking a larger protein segment encompassing both PHD domains. Full-length or truncated AIRE were expressed transiently in monkey COS cells and human primary fibroblasts using an SV40 promoter. For immunodetection of the AIRE protein, two polyclonal antisera were raised against synthetic peptides corresponding to the NH₂-terminal region and to the nuclear targeting signal (sp97179 and sp97181; see Example 6). Affinity-purified antibodies were tested on Western blots containing the 6x His-tagged recombinant AIRE fusion protein expressed in *Escherichia coli*. Both sp97179 and sp97181 antisera selectively recognized the His-tagged full length AIRE. Figure 5 shows a Western blot analysis of the expression of the AIRE constructs in transfected COS1 cells using antibody sp97181. The immunoblot revealed one strong immunoreactive band corresponding to the gene product of each construct. The size of the full length AIRE protein expressed in transfected cells was calculated at 58.8 kDa that is in agreement with the predicted molecular weight of 57.7 kDa. When cells were transfected with the truncated constructs AIRE-ΔSacI and AIRE-ΔBamHI, appropriate size bands were seen at 34.7 kDa and 23.5 kDa, respectively. No immunoreactivity was found in mock transfection nor in cells transfected with empty pSG5 vector. Similar results were obtained with sp97179 antiserum.

Immunocytofluorescence detection of the AIRE constructs expressed in COS cells was investigated 24 h and 48 h post-transfection by confocal laser microscopy and serial optical sections, after staining with antibodies sp97179 and sp97181. The staining pattern obtained

with sp97181 antiserum was essentially similar to that of sp97179. Only transfected cells showed a labeling with either of these antibodies indicating that COS1 cells are not expressing detectable endogenous AIRE. Mock or pSG5-only transfected cells showed no evident staining with either antisera. Immunofluorescence labeling as well as Western blot specific detection were blocked by pre-incubation of the antibodies with AIRE recombinant protein, further confirming the specificity of the antibodies. All experiments were performed in parallel with both antibodies and we will describe here data obtained using sp97181 antibody.

Example 11: Sub-cellular Localization of Wild-Type AIRE

COS1 cells transfected with the full length construct showed two populations of stained cells, one with a punctuate granular staining strictly restricted to the nucleus, as defined by YOYO-1 labeling of DNA, and a second one showing also a cytoplasmic expression of AIRE (Fig. 6). Transfection experiments carried out with either 2, 5, 10 or 20 µg of AIRE B1-1pA cDNA led to similar observations. When more than 300 transfected cells were analyzed, cytoplasmic staining was observed in approximately 70% of the cells whereas the AIRE expression was confined to the nucleus in the remaining 30%. In all of the cells where the staining was exclusively nuclear, the antibody reacted with punctuate structures. AIRE localized into small distinct speckles uniformly distributed in a given optical section of the nucleoplasm but excluded from the nucleoli (Fig. 6-I). Serial optical sections and confocal imaging showed that the nuclear labeling was present in domains representing approximately 5-8 µm of the nucleoplasm depth and thus localized within at least two-thirds of the nuclear volume. In cells where AIRE was expressed in the cytoplasm, the antibody decorated fibers spanning 4-8 µm of the cell depth that were arranged in a scaffold-like structure often forming bundles around the nuclear envelope (Fig. 6-II), reminiscent of the intermediate filaments of the cytoskeleton. This AIRE filamentous staining pattern was generally observed in conjunction with the characteristic nuclear speckles, albeit the nuclear staining sometimes consisted of fibrils spanning the nucleoplasm. Also, a few of the transfected cells were void of detectable labeling in the nucleus. No remarkable difference in the AIRE localization pattern could be noted between cells analyzed 24 h or 48 h after transfection.

To further authenticate the identity of the cytoskeletal filaments revealed by sp97181, additional transfection experiments were performed with COS1 or COS7 cell lines and human

primary fibroblasts. Cells were double-stained with sp97181 and a polyclonal antibody specific for vimentin (produced by standard techniques well known to the person skilled in the art). In COS cells expressing AIRE in the cytoplasm, both antisera decorated similar cytoplasmic fibers stretching from the nuclear envelope to the plasma membrane. Fig. 7-I shows that the AIRE and vimentin patterns are perfectly overlapping, demonstrating co-localization of AIRE with vimentin intermediate filaments. It should yet be noted that AIRE and vimentin appeared only partially overlapping in some of the transfected cells. Fig. 7-II shows the vimentin filaments of a cell expressing AIRE mainly in the nucleus, where the characteristic pattern appears composed of 50-100 speckles. In contrast, no evident punctuate nuclear staining could be observed in the cell shown in Fig. 7-I. Data strongly suggest that AIRE is a nuclear protein localizing to distinct functional sub-domains in the nucleoplasm but which may also be transiently stored in the cytoplasm during particular cellular stages. A similar dual cytoplasmic and nuclear AIRE staining pattern was observed in transfected primary fibroblasts. Fig 7-III shows here discontinuous cytoplasmic fibers arranged along vimentin intermediate filaments. Endogenous AIRE expression was not clearly detectable in fibroblasts either, and the AIRE sub-cellular localization pattern observed in both cell types was independent of the fixation method (see Example 8).

Example 12: Altered Cellular Localization of Truncated AIRE Products

The two N-terminal AIRE protein fragments expressed in COS cells or fibroblasts showed dramatic changes in their cellular distribution as compared with wild-type AIRE. The AIRE-DSacI construct expressing a 35 kDa protein truncated within PHD1 domain was also found localized in both cytoplasmic and nuclear compartments. In COS cells, cytoplasmic AIRE-DSacI showed at least in part co-localization with vimentin (Fig. 8-I) and often revealed fiber bundles around the nuclear envelope which were occasionally associated with small aggregates (Fig. 8-II). In contrast to wild-type, AIRE-ΔSacI protein showed a drastically altered nuclear sub-localization pattern. 24 h post-transfection, the mutant protein systematically localized in discrete nuclear domains consisting of intensely labeled foci, whereas no speckled pattern organization could be distinguished (Fig. 8-I and III). These intense nuclear dots were heterogeneous in size but often appeared as lipid-like round structures found as pairs but also as 3, 4 or multiple inclusions in the nucleoplasm, sometimes

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seen in the immediate vicinity of the nucleoli. These observations evoke similar structures referred as nuclear bodies, particularly coiled bodies. In some of the cells analyzed 48 h post-transfection, these nuclear inclusions were set against a very faint staining distributed diffusely in the nucleoplasm and excluding nucleoli. In human fibroblasts, similar observations were noted, though the nuclear inclusions were often significantly larger than in COS cells (Fig. 9-I); the cytoplasmic distribution was also found co-localizing with vimentin (Fig. 9-II).

The AIRE- Δ BamHI construct showed a strikingly different sub-cellular localization as compared with full-length AIRE and AIRE- Δ SacI. This truncated protein of 23.5 kDa presented a drastically impaired cytoplasmic distribution pattern where fibers could never be observed in any of the COS cells expressing AIRE- Δ BamHI. Instead, large cytoplasmic aggregates were commonly concentrated in the perinuclear region (Fig. 10-I) or at one pole of the nucleus (Fig. 10-II), albeit sometimes dispersed in the cytoplasm (Fig. 10-III). The same construct expressed in fibroblasts could also form cytoplasmic aggregates (Fig 11-I), but interestingly the mutant protein has retained the ability to co-localize along vimentin intermediate filaments in this cell type. Nonetheless, AIRE- Δ BamHI and vimentin staining revealed unusual wavy filaments that were never observed otherwise (Fig. 11-II). Besides, COS cells and fibroblasts containing large aggregates of the AIRE- Δ BamHI protein generally presented a dramatically altered distribution of the vimentin intermediate filaments (Fig. 10-III). This is particularly exemplified in the cell shown in Fig. 11-I, where vimentin appears trapped within AIRE aggregates rather than being organized in filaments. This evokes the hypothesis that protein-protein interactions involved in maintaining the shape and integrity of intermediate filaments are impaired in cells overexpressing AIRE- Δ BamHI. The nuclear staining showed a confined pattern comparable to that of the AIRE- Δ SacI truncated protein as indicated in Fig. 10-I. Intensely labeled discrete foci appearing as pairs or as multiple dots with a typical diameter of about 1 micron were observed at 24 h or 48 h post-transfection. Orthogonal sections of such nuclear inclusions indicate rod-like structures spanning 2-5 μ m in the nucleoplasm depth. However, no diffuse or speckled nuclear staining could be seen at 24 h nor 48 h post-transfection.

Importantly, these data showed that deletion of the one-third C-terminal part of AIRE containing the PHD motifs abolished the normal nuclear distribution. The question whether the PHD zinc fingers directly mediate the correct protein localization to specific nuclear

domains was not addressed here. The truncated proteins retained the ability to be targeted to the nucleus since they contain the NLS domain. However, the two deletion mutants are mislocalized in the nucleus when lacking an element conferring speckled punctuate pattern and located between residue no. 306 and the C-terminus.

Example 13: Isolation of the mouse *AIRE* gene

Briefly, mouse homologues of the human *AIRE* gene were isolated by cross-species hybridization of mouse genomic libraries with a human cDNA probe containing the complete *AIRE* coding sequence. Six positive mouse clones (PAC RPCIP711H2150, P1's ICRFP703A23152, A10129, G23152 and J2183, and cosmid MPMGc121L12287) were isolated from the screenings and were analyzed further by restriction digest mapping and southern hybridization analysis.

In detail, the mouse homolog of the human *AIRE* gene was isolated by cross-species screening of various mouse genomic libraries with a human cDNA containing the complete *AIRE* coding sequence (see Figure 2A, referred to as *hAIRE*). Six positive clones were isolated and analyzed by restriction digest: 1 PAC (RPCIP711H2150), 4 P1s (ICRFP703A23152, A10129, G23152 and J2183) and 1 cosmid (MPMGc121L12287). When hybridized with *hAIRE*, all clones showed 4 *Eco*RI fragments totaling a size of 20,6 kb excepted for A10129 showing an *AIRE Eco*RI pattern of 13,54 kb. Hybridizations with the most 5' end or 3' end of *hAIRE* indicated that A10129 was missing at least the first exon, whereas the 5 other genomic clones contained the complete *AIRE* coding sequence. Cosmid MPMGc121L12287 was chosen for genomic sequencing. The mouse *AIRE* exons were mapped by restriction mapping and Southern hybridization of cosmid L12287 with individual human exons. The gene organization was characterized further after examination of the complete genomic sequence and comparison with *AIRE* mouse cDNA sequence.

Example 14: Restriction digests and southern hybridization analysis

DNA from the mouse *hAIRE* positive clones were digested with *Eco*RI and *Hind*III restriction enzymes (New England Biolabs) according to the manufacturer's recommendations. Digested DNA was separated by 1-1.5% agarose gel electrophoresis and transferred onto Amersham

Hybond-N+ nylon membranes. Full-length *hAIRE* probes and probes corresponding to either the most 5' end or the 3' end of *hAIRE* were generated by PCR. Southern hybridizations were carried out overnight at 42°C in hybridization mix consisting of 5x SSPE, 5x Denhardt's solution, 50% Fluka formamide, 1% SDS and 0.05 mg/ml of denatured salmon sperm DNA. Filters were washed in 2 changes of 2x SSC each for 10 minutes at 42°C, then in 2 changes of 2x SSC/0.1% SDS, the first for 15 min at 42°C and then a final wash for 20 minutes at 65°C. Filters were exposed at -70°C to Kodak X-OMAT AR imaging film with a single intensifying screen for several hours to overnight, depending on the intensity of signals.

Example 15: Human and mouse RT-PCR analysis

Human: RT-PCR analysis was performed on Clontech's Human Immune System Multiple Tissue cDNA Panel of first-strand cDNA from the following tissues: human bone marrow, fetal liver, lymph node, peripheral blood leukocyte, spleen, thymus and tonsil. Primers B127FR4-21 (5'-GGC TTC TGA GGC TGC ACC) and B127FR4-29 (5'-GCT CTG GAT GGC CTA CTG C) were used to amplify a 1.6 kb region specific for *hAIRE*. Each PCR was performed in a 50 µl reaction mix containing 5 µl of MTC Panel cDNA, 10-20 pmol of each primer, 1 µl of a 10 mM dNTP mix, 5 µl of Perkin Elmer *GeneAmp*™ 10X-PCR buffer (100 mM Tris-HCl pH 8.3; 500 mM KCl; 15 mM MgCl₂; 0.01% w/v gelatin), and 3 µl of freshly prepared 28:1 (7 mM:1.4 mM) mixture of TaqStart Antibody (Clontech) and *AmpliTaq*™ DNA Polymerase (Perkin Elmer). PCR reactions were performed in a Biometra UNO II thermocycler beginning with a 2 min initial denaturation step at 94°C, followed by 38 cycles of 94°C for 45 sec, 56°C for 40 sec, 72°C for 1 min, and a final extension step at 72°C for 5 min. Products of the PCR were re-amplified with nested primers B127FR4-17 (5'-AGA AGT GCA TCC AGG TTG GC) and B127FR4-33 (5'-GTG TGC TCG CTC AGA AGG G) to confirm that the products were specific to *hAIRE*.

RT-PCR amplification with primers B127FR4-21 and B127FR4-29 was also performed on human marathon tissues isolated from lung, muscle, testis, hindbrain, and spinal cord following the PCR conditions described above.

Mouse: Mouse primers Mforw4 (5'-TGG CAG GTG GGG ATG GAA) and Mrev15 (5'-GGA GGG ATG GAA GGG GAG GA) were used to amplify AIRE specific regions from Clontech's Mouse Multiple Tissue cDNA Panel 1 (consisting of first-strand cDNA from

mouse heart, brain, spleen, lung, liver, skeletal, kidney, testis and 7-day, 11-day, 15-day and 17-day embryo tissues). PCR reaction mixtures were set up according to the same conditions described for human RT-PCR's, with the exception of using mouse specific primers and a PCR annealing temperature of 63°C.

Example 16: Chromosomal localization of mAIRE

Chromosomal localization of mAIRE was established by PCR analysis of mouse chromosomes 3, 10 and 17. PCR amplifications were performed using mouse specific primers Mforw2 (5'-TCC CAC CTG AAG ACT AAG C) and Mrev32 (5'-TCA CAG CTC TCT GGA CAG AA) on cell hybrids SN11CS3 (chromosome 3), SN17C3 (chromosome 10) and EJ167 (chromosomes 17 and 3 on a human background). PCR reactions were performed in 30 µl volumes containing 5 µl of mouse chromosomal preparations, 10-20 pmol of each primer, 1 µl of a 10 mM dNTP mix, 5 µl of Perkin Elmer *GeneAmp*™ 10X-PCR buffer, and 3 µl of freshly prepared 28:1 (7 mM:1.4 mM) mixture of TaqStart Antibody (Clontech) and *AmpliTaq*™ DNA Polymerase (Perkin Elmer). PCR reactions were performed in a Biometra UNO II thermocycler beginning with a 2 min initial denaturation step at 94°C, followed by 35 cycles of 94°C for 45 sec, 51°C for 40 sec, 72°C for 2 min, and a final extension step at 72°C for 5 min.

Example 17: PCR products

Products from PCR amplifications were purified using the Qiagen QIAquick PCR Purification Kit or Clontech Chroma Spin+TE columns. Purified products were then checked by 1.5% agarose gel electrophoresis and sequenced.

Example 18: Genomic Sequencing

The cosmid DNA was isolated using a standard lysis method (Birnboim and Doly 1979) and purified on a CsCl-gradient (Radloff et al. 1967). The closed circle band was sonicated, size fractionated and ligated into M13 vector (Craxton 1993). M13 templates were prepared by the triton method (Mardis 1994). The shotgun sequencing was performed using Thermo

Sequenase (Amersham) and dye-terminator chemistry (Perkin Elmer). Data were collected using ABI 377 automated sequencers and assembled with the gap4 (Staden 1996). Gaps were closed by resequencing the M13 templates with ET dye primers (Amersham).

Computer Analysis: Genome-wide repeats were identified with the Repeatmasker program (A.F.A Smit and P. Green at <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). The GC content and distribution was determined with the LPC algorithm (Huang 1994). Homology searches against various databases were performed using BLAST version 1.4 (Altschul et al. 1990) and FASTA version 2.0 (Pearson and Lipman 1998). Programs GAIL2 (Urbacher and Mural 1991), XPOUND (Thomas and Skolnick 1994), MZEF (Zhang 1997) and GENSCAN (Burge and Karlin 1997) were used for exon prediction. Promoter predictions were done with „Promoter Scan II“ (Prestridge 1995) and „Transcription Start Site“ using both Ghosh/Prestridge (TSSG) and Wigender (TSSW) motif databases (V.V. Solovyev, A.A. Salamov and C.B. Lawrence at <http://dot.imgen.bcm.tmc.edu:9331/gene-finder/gf.html>).

Example 19: Comparative genomic sequencing

Cosmid L12287 was completely sequenced (46,8872 bp long; EMBL accession no. AF073797) and the data were compared with the human *AIRE* gene locus that we have previously sequenced (36,284 bp, accession no. HSAJ9610). Automatic sequence analysis of clone L12287 was performed with the Rummage software (http://www.genome.imb_jena.de). Gene prediction programs detected the *AIRE* gene and revealed also an incomplete gene model located 6 kb from the 5' end of *AIRE* that was corroborated by anonymous EST matches (e.g. accession no. AA413561). Interestingly, one of the anonymous exons showed high homology with a trapped exon (HC21EXc32; D86111) mapping to human chromosome 21q22.3 (Genebank Accession no. D86111) This confirmed the high degree of conserved syntenicity between mouse and human in this region.

The mouse *AIRE* gene structure was initially deduced by comparison of the genomic sequence with that of the h*AIRE* human cDNA. Sequence analysis confirmed that cosmid L12287 contained the complete *AIRE* coding sequence consisting of 14 exons spanning 13,276 bp from the proposed initiation codon to the termination codon, which compares with 11,714 bp for the human gene (Fig. 12). The mouse *AIRE* intron/exon boundaries were confirmed experimentally after alignment of mouse cDNA and genomic sequences. Data are summarized

in Table 2A and 2B. In both species, splice acceptor and splice donor sequences were found to conform to the GT-AG rule, and the intron phase is completely conserved. Sizes of coding exons ranges from 63 to 181 bp in human, versus 69 to 177 bp in mouse. The GC content of the mouse AIRE coding sequence is 61% whereas that of the human is 67,7 %. The overall nucleotide sequence identity between the mouse *AIRE* coding sequence and that of the human is 76.67 %.

A TATA box was found in a conserved position less than 200 bp upstream of the putative translation initiation site, at position 9,413 and 22,486 of the mouse and human sequences, respectively. A CpG island was identified immediately upstream of the AIRE gene in both species (see Fig. 1). In order to detect potentially conserved regulatory regions, sequence comparison was represented in a dot-matrix using the dotter program (Erik L.L. Sonnhammer and Richard Durbin, Gene 167:GC1-10 (1995)) (Fig. 13A). The plot shows clear identification of exons 1 to 11 and of the terminal exon, whereas exons 12 and 13 are below threshold indicating higher sequence divergence for these 2 exons (Fig. 13A). Interestingly, a conserved region of approximately 100 nucleotides was identified 3 kb upstream of the AIRE first exon suggesting that this region may be potentially relevant to the expression of the AIRE gene (Fig. 13B).

Example 20: Localization of the mAIRE gene to chromosome 10

Comparative mapping between mice and human has shown that human chromosome 21q22.3 shares conserved synteny with mouse chromosomes 10 and 17. Then, the chromosomal localization of AIRE was determined by PCR analysis of monochromosomal hybrids containing mouse chromosomes 10 or 17. A primer set derived from the genomic sequence (see Example 16) amplified a specific band in total mouse genome and chromosome 10. Fig. 15 demonstrates that this fragment is mouse-specific and different to that amplified in human DNA. Data are consistent with the expected conserved synteny in this region.

The predicted mouse AIRE protein (mAIRE) is 552 residues and has a calculated pI of 8.43 and a theoretical molecular weight of 59 kDa. The overall identity between the mouse and human AIRE proteins is 72,37 % and similarity is 74,58 %. The two proteins are remarkably conserved and harbor the modular domains described for the human protein. These features include a N-terminal LXXLL motif located in a putative helical region that is a signature for

nuclear receptor binding, a nuclear targeting signal, a SAND domain that was recently described as potential DNA binding domain, and two PHD-type zinc finger motifs (Fig. 16). Essential residues are conserved between the two species. The two proteins are likewise proline rich (11 %) and have a predicted globular secondary structure. AIRE possibly encodes for a chromatin-associated transcription factor on the basis of its functional attributes shared by other nuclear PHD zinc finger proteins involved in transcriptional control.

Example 21: AIRE gene expression

AIRE transcripts were detected by PCR amplification from mouse cDNAs derived from a wide range of tissues. Sequenced PCR fragments confirmed the presence of AIRE cDNAs in ES cells, 11 days embryo, spleen, lung, heart, skeletal muscle and testis. The complete mouse cDNA sequence was deduced from overlapping PCR fragments amplified in ES cells. Evidence for 3 alternatively spliced isoform transcripts was also observed and these were designated type I, II and III. One variant found present in ES cells corresponds to skipping of exon 10 (Type I; Fig. 17A). If translated, variant type I would lead to a protein with only a small spacer between the two PHD fingers. A second splice variant found in ES cells and testis correspond to a 3 bp deletion in the splice acceptor site in exon 8, leading to a shorter exon 8 (Type II; Fig. 17B). The predicted protein for type II is similar to canonical AIRE with only with a missing lysine at the beginning of exon 8. The third splice variant that was observed in 11 days embryo, heart, testis and spleen was a 12 bp shorter exon 6 consecutive to a change in exon 6 splice donor site (type III; Fig. 17C). The predicted peptide is 4 residues shorter at the end of exon 6 as compared to normal AIRE. In ES cells, type III was observed in combination with variant type II or in a combination with the types I and II in the same cDNA molecule.

Expression of human AIRE was assessed in a panel of cDNA from various immunological tissues (Fig. 18). Sequenced PCR products indicated that AIRE was expressed in fetal liver, lymph node, peripheral blood leukocyte, thymus, bone marrow and spleen. Interestingly, the splice variant type II described above was also found in two human tissues, spleen and bone marrow. However, the data did not address whether alternative splicing leading to the two other variants was conserved between the two species.

TABLE 1 Mutations in the APGD1 gene

<u>Mutation</u>	<u>No.</u>	<u>Exon</u>	<u>Nucleotide</u>	<u>Haplotype</u>	<u>No.</u>	<u>Consequence</u>
$C_{889} \rightarrow T_{Fin\ major}$	1	6	889	(4 3 5 1 2)	1.1	Arg -> STOP, truncated 256 aa protein
				(4 4 7 4 5)	1.2	
				(5 4 2 2 5)	1.3	
				(5 4 5 4 3)	1.4	
4 bp insertion	2	8	1086-1089	(5 3 5 3 3)	2.1	frame shift, truncated 371 aa protein
13 bp deletion	3	8	1085-1097	(4 5 5 4 5)	3.1	frame shift, truncated 372 aa protein
A insertion	4	10	1284	(5 4 3 2 5)	4.1	frame shift, truncated 422 aa protein
C deletion	5	10	1313	(2 10 7 4 5)	5.1	frame shift, truncated 478 aa protein

Tabelle 1

Table 1 summarizes the mutations and the predicted consequences for the APGD1 putative protein. The APGD1 exons were amplified with intronic primers and initially screened by the SSCP method (Orita, M., et al., *Proc. Natl. Acad. Sci. USA*, 86, 2766-2770 (1989)). Detected changes were characterized by solid-phase sequencing (Syvänen, A. C., et al., *FEBS Lett.*, 258, 71-74 (1989)). The haplotypes of the disease chromosomes were constructed from alleles of the markers shown in figure 1A (cen - JA1, D21S1912, PFKL(CA)_n, PB1, D21S171 - tel). Haplotype 1.1 is the major haplotype in Finland (Fin major). Haplotypes 1.2 (Italian), 1.3 (German) and 1.4 (German) carry the same mutation as the major Finnish allele. Haplotypes 1.3 and 1.4 are most probably of the same origin since they share the same centromeric alleles. An Italian patient was homozygous for haplotype 2.1 and mutation 2. Haplotype 3.1 was observed as homozygous in one Dutch and in two British patients, and as heterozygous in one German patient. All chromosomes carrying this haplotype have mutation 3. Two Finnish patients were compound heterozygotes for haplotype 4.1 and for mutation 4. Haplotype 5.1 and mutation 5 were found homozygous in a French patient. The detected mutations were monitored against a control panel (see text) by minisequencing (Syvänen, A. C., et al., *Am. J. Hum. Genet.*, 52, 46-59 (1993)) (mutations 1, 4 and 5) or by size separation of radioactively labeled PCR products on denaturing PAGE (mutations 2 and 3). None of these mutations were detected in a homozygous form in the control subjects. The carrier frequency of the Fin major mutation was observed to be 1:250 in the Finland. This mutation was also found in a heterozygous form in one CEPH parent whereas we did not detect any carriers for the other mutations.

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Exon	Size (bp)	Position in cDNA	Position in genomic DNA	Intron size (bp)	Splice acceptor	Splice donor	Intron phase
1	132	121-252	22648-22779	418	5' UTR	CAGgtggg	0
2	175	253-427	23198-23372	246	tgcagGAG	AAGgtggg	1
3	156	428-583	23619-23774	383	tgcagATG	CAGgtacc	1
4	75	584-658	24158-24232	753	tcagGCT	ACGgtgag	1
5	112	659-772	24986-25099	1198	cccagGGA	CAGgtaga	1
6	144	773-918	26298-26443	185	cccagGCG	CCCgtaag	0
7	81	919-999	26629-26709	1026	tgcagGGT	CAGgtaat	0
8	116	1000-1115	27736-27851	1091	gccagAAG	CAGgtgag	2
9	100	1116-1215	28943-29042	590	agcagTGG	CCGgtatg	0
10	181	1216-1398	29633-29815	612	tccagCTC	CAGgtgag	0
11	122	1399-1520	30428-30549	490	cacagAAC	CGGgtgag	2
12	103	1521-1623	31040-31142	1879	tgcagGAC	AAGgtcag	0
13	63	1624-1686	33022-33084	1206	tccagGAT	GAGgtaac	0
14		1687-1755	34291-34359		cgcagCAC	3' UTR after stop	

human *AIRE* gene structure information

Numbering of exon 1 begins from translation start site (A of ATG start codon is position 1): Numbering of exon 14 ends at the stop codon. The exon location in the cDNA sequence correspond to EMBL accession no. Z97990, and the exon location in the genomic sequence correspond to GenBank accession no. ? WEB C.741.

Tabelle 2A

Exon	Size (bp)	Position in cDNA	Position in genomic DNA	Intron size (bp)	Splice acceptor	Splice donor	Intron phase
1	135	1-135	9555-9689	312	5' UTR	CAGgtggg	0
2	175	136-310	10002-10176	229	tgcagGAG	AAGgtggg	1
3	156	311-466	10406-10561	381	tgcagATG	CAGgtaca	1
4	75	467-541	10943-11017	447	cgcagGCT	ACGgtgag	1
5	114	542-655	11465-11578	1420	tccagGAA	CAGgtaaa	1
6	149	656-804	12999-13147	188	cccagGAA	CCTgtaag	0
7	81	805-885	13336-13416	1674	catagGGT	CAGgtaag	0
8	116	886-1001	15091-15206	1088	gtcagAAG	CAGgtaag	2
9	100	1002-1101	16295-16394	851	cacagTGG	CCGgtagt	0
10	177	1102-1278	17246-17422	949	tccagATC	CCAggtgag	0
11	122	1279-1400	18372-18493	96	tgcagGGT	GGGgtgag	2
12	109	1401-1509	18590-18698	2491	gacagGAC	AAGgtcag	0
13	69	1510-1578	21190-21258	1492	tccagGTA	GAGgtaat	0
14	78	1579-1656	22751-22828		ctcagCAC	3' UTR after stop	

mAIRE gene structure information

Numbering of exon 1 begins from translation start site (A of ATG start codon is position 1): Numbering of exon 14 ends at the stop codon. The exon location in the cDNA sequence correspond to EMBL accession no. ???, and the exon location in the genomic sequence correspond to GenBank accession no. AF073797.

Tabelle 2B